

Input file 57h8Bcons; Out File 57h8Btra
Sequence length 3076

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CTGGCCACGTCGCCCTGGGTGACCTTCCTCGGATGCAGAATCCGCCCCTGCGAGCATCCTCTTCCTCCTAGGCTCTGAA
GGCCCGGGGAGCGTGAGCGATGCCCAGCTGCACCCGGGCAGGGCTCGCCTTTGTTTGCCAGTAAGGAGGAGAGGCTGTC
TCAGCTGCAGAGGGGTCATCCCTGCTTCAAGCCAGTGCCTCTTCCCAGCTCCC ATG GGG ACC ACC GAA GCC
M G T T E A
T L R M E N V D V K E E W Q D E D L P R
ACG CTC CGG ATG GAA AAC GTG GAC GTG AAG GAG GAA TGG CAG GAC GAA GAT CTT CCC AGG
P L P E E T G V E L L G S P V E D T S S
CCA CTC CCA GAA GAG ACG GGG GTG GAA CTG CTT GGC AGC CCG GTG GAA GAC ACA TCC TCT
P P N T L N F N G A H R K R K T L V A P
CCT CCC AAC ACG CTA AAT TTC AAC GGA GCG CAT CGT AAG AGG AAG ACG CTG GTG GCC CCA
E I N I S L D Q S E G S L L S D D F L D
GAG ATC AAC ATT TCT CTG GAT CAG AGT GAG GGG TCC CTG CTG TCC GAT GAC TTC TTG GAT
T P D D L D I N V D D I E T P D E T D S
ACC CCT GAT GAC CTG GAT ATT AAC GTG GAT GAC ATC GAG ACC CCC GAT GAG ACC GAC TCG
L E F L G N G N E L E W E D D T P V A T
CTG GAG TTC CTG GGG AAT GGC AAC GAA CTG GAG TGG GAA GAC GAC ACC CCC GTG GCC ACC
* A K N M P G D S A D L F G D G T T E D G
GCC AAG AAC ATG CCC GGG GAC AGC GCG GAT CTA TTT GGG GAC GGC ACG ACG GAG GAC GGC
S A A N G R L W R T V I I G E Q E H R I
AGC GCC GCC AAC GGG CGC CTG TGG CGG ACA GTG ATC ATC GGG GAG CAA GAG CAC CGT ATA
D L H M I R P Y M K V V T H G G Y Y G E
GAC CTG CAC ATG ATC CGG CCT TAC ATG AAA GTG GTC ACC CAC GGA GGG TAC TAC GGC GAA
G L N A I I V F A A C F L P D S S L P D
GGC CTC AAC GCC ATC ATC GTC TTC GCA GCC TGC TTC CTT CCA GAC AGC AGC CTC CCC GAC
Y H Y I M E N L F L Y V I S S L E L L V
TAC CAC TAC ATC ATG GAG AAC CTC TTC CTG TAC GTC ATC AGC AGC TTA GAG CTC CTG GTG
A E D Y M I V Y L N G A T P R R R M P G
GCT GAG GAC TAC ATG ATC GTG TAC CTG AAC GGT GCC ACG CCC CGG CGG AGG ATG CCT GGA
I G W L K K C Y Q M I D R R L R K N L K
ATC GGC TGG CTG AAG AAG TGC TAC CAG ATG ATC GAC CGG AGG TTG CGG AAA AAC CTG AAG
S L I I V H P S W F I R T V L A I S R P
TCC TTG ATC ATC GTC CAC CCC TCG TGG TTC ATT CGG ACT GTG CTG GCC ATC TCT CGC CCT
F I S V K F I N K I Q Y V H S L E D L E
FTC ATC AGC GTC AAG TTC ATC AAC AAG ATC CAG TAC GTG CAC AGC TTG GAA GAC CTG GAG
Q L I P M E H V Q I P D C V L Q Y E E E

FIGURE 1

CAA CTC ATC CCT ATG GAA CAC GTC CAG ATC CCA GAC TGC GTC CTG CAA TAC GAA GAG GAA
 R L K A R R E S A R P Q P E F V L P R S
 AGA CTG AAG GCC AGG AGG GAG AGC GCG AGG CCC CAG CCG GAG TTT GTG CTG CCC AGG TCT
 E E K P E V A P V E N R S A L V S E D Q
 GAA GAG AAG CCA GAG GTG GCA CCA GTG GAA AAC AGG TCT GCT CTG GTC TCA GAA GAT CAG
 E T S M S *
 GAA ACA AGC ATG TCC TGA

GGCGACGTGAGCATAACAAAGGACATGGAAGAAGATTCCAGATGCCAGAAAACCTCTGTGACAGCGCCCACTGGCCCCAG
 ATCTCATCCTGCCTCATCCTGAGTCCCAATCTTCCAAGGGTGCCAGCCCCCTCCGTTTCATCTCTGAAACCCAGCATCCTT
 TTCAGCTGCTTGAAAACATTGTATTTTTTTTTTTTAAACGATGCAGTATTTGTGCGTTCCAGAAAAGGGCCCAGCTCTGA
 GCCCCCTCACCTTCCACACTCACGAACTCTCAGCCGAGGAAGGCAAGAAGCGCAGGGGGTGCCCCGCGTGGCGTCGGTG
 GCCTCCGCTCCTGCTCGCAGCCCCCTGTGGTCAGAGCTGGATACAAGATTCAAGACCCCTTCTCTTGCTTGTACCCGCTC
 CAGGTTGGAGCCACAGACACCCACCGCCACCCCGGCTGGGTCTGCGTCCTTTCCTGTGCCTTTCCTCCAGAATGCGGC
 CTCAGACCTAGAAGCTCAACCCCCCTATGAGGGCCACGTCTGGGGTAGCTCCTGACCTCCGACCTTATGTCCAAATTT
 CACACCCATGGTTTTTTCATTTGACCCGCCCCCTTCTCGCTCATAATGACACCCAGCTCCTTTGAGAGGATCAGAGCCCA
 TTGCACAAGAAGAGCCGCTGCCAACCATCCTTGTCTCCGATTGCAAAATGACACCCAGTAATCTAGAACATTCTCAA
 GCCCCTTTAACTCAGATGTCAAGCCACCGGGCAAACCCCGTCAATACCTCCACCAAGGAATGAGATATGTGGACCTCA
 CTGCTCCCCCAACCCAGCGTCAGGCTGGGACACGCCAACGCTGTTCCGGGTTGGAACAGCACAGGCTCAGAACTGGCT
 CTGAAATAGGCAGACCTAGCAAGAGGAAGATACAGGGTATCGGGCGTTTGAGTGTTTCAGAAGTCATTTCGGGAAGATAA
 ATCCAGTGCGCTGGCCGCAGCCACCTGCATTCAAAGCTTGACCAGCGGGTTCTTGTTTCGGGAGGCAAATTTCCCTAGG
 AAAAAGAAGACAGACTTTTCTAATGGGGTCCAAATGCGGATCACTGGTCAGATGGACTCTAGAAGCACTGAGCTCCCTG
 TCTCTGGAAGTATTTAAGAAAAGGCTGGGCCAGGCACGATGGCTCACGCCTGTAATCCCAGACTTTGGGAGGCCGAGGC
 AGGCGGATCACCTGAGGTGAGGAGTTTGAGAACAGCCTGGCCAACATGGTGAAACCTCATCTCTACTAAAAATACAAAA
 ATTAGCCAGGCGTGGTGGCAGGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCATGAGAATCACTTAAACCTGAGA
 GGCAGAGGTTACAGTGAGCCAAGATCGTGCCACTGCATTCCAGCCTGGGCGACAGAGCAAGACTCTGTCTCAAAAAAAAA
 TAAAAAATAATCAGGGCACAGTGGCTCATGCCTGTAATCCCAGCACTCTGGGAGGCTGAGGTGGGTGGATCACCTGAGG
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 GTGCATGCCTG

FIGURE 1 (cont'd)

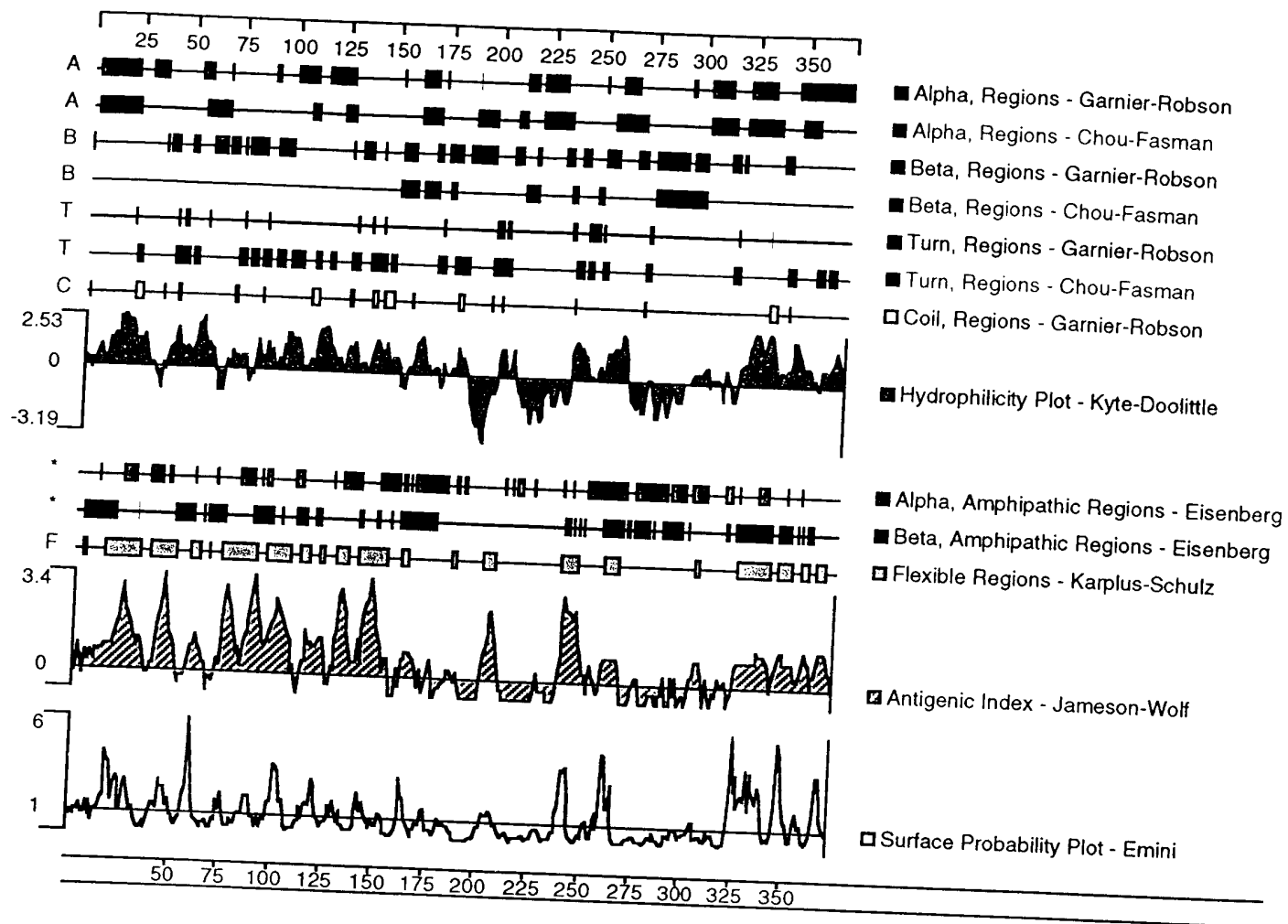


FIGURE 2

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GTCGACCCACGCGTCCGCGGAA M E E E T E F L E L G T R I
ATG GAG GAG GAG ACA GAG TTC CTT GAG CTC GGA ACC AGG ATA
S R P N G L L S E D V G M D I P F E E G
TCA AGA CCA AAT GGA CTA CTG TCA GAG GAT GTA GGA ATG GAC ATC CCC TTT GAA GAG GGC
V L S P S A A D M R P E P P N S L D L N
GTG CTG AGT CCC AGT GCT GCA GAC ATG AGG CCT GAA CCT CCT AAT TCT CTG GAT CTT AAT
D T H P R R I K L T A P N I N L S L D Q
GAC ACT CAT CCT CGG AGA ATC AAG CTC ACA GCC CCA AAT ATC AAT CTT TCT CTG GAC CAA
S E G S I L S D D N L D S P D E I D I N
AGT GAA GGA TCT ATT CTC TCT GAT GAT AAC TTG GAC AGT CCA GAT GAA ATT GAC ATC AAT
V D E L D T P D E A D S F E Y T G H D P
GTG GAT GAA CTT GAT ACC CCC GAT GAA GCA GAT TCT TTT GAG TAC ACT GGC CAT GAT CCC
T A N K D S G Q E S E S I P E Y T A E E
ACA GCC AAC AAA GAT TCT GGC CAA GAG TCA GAG TCT ATT CCA GAA TAT ACG GCC GAA GAG
E R E D N R L W M T V V I G E Q E Q R I
GAA CGG GAG GAC AAC CGG CTT TGG ATG ACA GTG GTC ATT GGA GAA CAA GAG CAG CGC ATT
D M K V I E P Y R R V I S H G G D S G Y
GAC ATG AAG GTC ATC GAG CCC TAC AGG AGA GTC ATT TCT CAC GGA GGA GAT TCA GGA TAC
Y G D G L N A I I V F A A C F L P D S S
TAT GGG GAC GGT CTA AAT GCC ATC ATT GTG TTT GCC GCC TGT TTT CTG CCA GAC AGC AGT
R A D Y H Y V M E N L F L Y V I S T L E
CGG GCG GAT TAC CAC TAT GTC ATG GAA AAT CTT TTC CTA TAT GTA ATA AGT ACT TTA GAG
L M V A E D Y M I V Y L N G A T P R R R
TTG ATG GTA GCT GAA GAC TAT ATG ATT GTG TAC TTG AAT GGT GCA ACC CCA AGA AGG AGG
M P G L G W M K K C Y Q M I D R R L R K
ATG CCA GGG CTA GGC TGG ATG AAG AAA TGC TAC CAG ATG ATT GAC AGA CGG TTG AGG AAG
N L K S F I I V H P S W F I R T I L A V
AAT TTG AAA TCA TTC ATC ATT GTT CAT CCA TCT TGG TTC ATC AGA ACA ATC CTT GCT GTG
T R P F I S S K F S S K I K Y V N S L S
ACA CGA CCT TTT ATA AGT TCA AAA TTC AGC AGT AAA ATT AAA TAT GTC AAT AGC TTA TCA
E L S G L I P M D C I H I P E S I I N I
GAA CTC AGT GGG CTG ATC CCA ATG GAT TGC ATC CAC ATT CCA GAG AGC ATC ATC AAT ATT
D L K L K E K P *
GAC TTG AAG CTG AAA GAA AAG CCT TAG

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TTGGCCATGCTGGAAGAAGAGGATGCTTTTCTGGTTCATGGTTCTGTTGAAACATATCTACCTGAAAGAGACAGGGCTG
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AAGATATTTTATGAAATTGTGTGTACTTTCCTATTTTGCCAATTATGTGCCTCAAAGATTTTAGTTGAGCCTTAGCAAG

```

FIGURE 3

AAAGTAGGACCTTCCATTTCAATAC●●●ATTAACACGGTGTAGTGATACTTGT●●●CTTAGACTGGTGTTTACCAGTAA
 GATACCTTTAATCCACTGTTAAGTATGAGTGGATTTGTTTCCATAGATTAGCTGGATTTCCCTTTTGGTGATTGCATTAG
 GTTTAAAGTACACAGGTCTCAACTCTCCCCAGGAAAGTTTCCCCTGTTTGACTCCACCTTTAAAATCCTAAGCCTGACT
 AGGACAGCCACAAACCACACAAGGTGTAAAACCATCATCAGCTAAGTGCCCGTTTTGTTCTTGTTTACCAGAATCTCCT
 TTAAGTTCTCAAAGGGAAGCCGGGCTTTCTAATCCACGTCAACTTTATTTTAGTTGTCAAATTGGGCATTATATTTTAT
 GTAAATTGGTCTTTTAACATCATTTTCTGATGAATGTTGGTGACCACCACATTGTGAAATTTAAGAATCCGTGTTGCA
 TGTTTGGTAGCTCTCTGAGTTTCAGGCCATAAACTCAGCTCCAGAGGTTACCTTTTAAGTGCCAAGAACTCAAGTGCAA
 GGTGGCCTACTCAAAAATCATTGTTGGTAGCATTGAGTTATTCATGAATTCCTCTCTCGCATGCATTATAAAAAGTGATCT
 GCTTTAAACACCGTAATCTGATCATAGGCTTAAATTAATATGAGTATTACTTTCATGTACAAAATATTTCCCTTTAT
 AGTCTTCATATGCCCTTTAAATGCCAACAAGATTTCAAGTCTGTAGGCCTCTAGTGAGGTGGGGTGGCAAACCACAGC
 TAAGTCTCGCTCACCCTGCAAGCTAAGAATGGTTTTTTACATTTTGGGTGGAAAAATTTTTTTGAATATTTTCATGAC
 ACATGAAAATTATTCAAATGTTAGTGCCGATAAATAAAGTGGTACTGAAACACAGCCACACAACTTGTTTTTGTACTG
 TCTACAGCTACTTTCACACTACAGCCGCAGAGCTGAGCAGTTCAGCAGACCGTATGTCCACAAATGCCTAAAACATTGA
 CTATGTTTACAGAAAAAGTTTGCTGACCCCTGCTCTAGCAAACGCATCCTTTCTACTCCACCCCAATTTGTATTTAGA
 TAGTTTCTCTAACAGAACGGACAAATGAGGCTGCAAACTAATTTATTTTGTCAAAAATCAATGTTTTGACATCCACAG
 ACAGTGAAATAAAAGAAATGGCTTGCTGAAAAACATGAGGAGTCCTAGCCACAAAATCACTGCTTAGGTTGCAATTGCC
 肺 AAAATGAAGCCTTCTTAGAAGCACTTCTTTAGTATATACAGGTGTTGGCTGAAGTCCGTGCCTCACTCTGGGAACCATT
 CTTAGTCTCCAGTGTCTCCTATTACAAAGAAGCTGGCAGAAATAAAAATGAAGGGGTGAGAGCGGTTCACCCCTAGTCT
 CATGGTGGAAAAATTCATTGGGGAGAGCTGTCCAGGATATTTGGAGTCCTGGGTAGAAGGAGCTTGTAACACTTTAAAG
 TCGACATCTTTGCACAGGTGATTGAGTTTCTCTGACCTCATTGCTTCACCTCTGTCTCCTCCCGTCCTTCCGCACGTGC
 CCACACACACGCAGTTCAGCCCTCTTTCCTCCATAAGCCTCCATCGTTTTCTCTTTTCTCCTCTTGATCCTTTCAAGCG
 AGTATCTTGTTGAATTGTATGTTCTGTTGGATCTCCTCCTTCATAACATCTGGCTTGTTGGACAGAAAAACCCTACAGC
 CCACCCCTCCACAGCCACCTCCACTTTTGAAAGCCCAAATTACACCTCTCCAGAACACAGTGTTGACGTAAATAC
 AGTTACCCAATATTCCTGTTTGTTCACCTATTTGCTACTTTCACCTCAGTAGCATCCCATTTTGTAATAATGAATTCCATG
 GTCACCCTGTCACAGGAAGTAATGAAAAATCCAGTGTTGAGTGAGTGGTGCAAACCTGAGGGCATAGAGCTGTTTATA
 GAGGGCTCTTGTTATAGCCAAACAGACACAGCAACAATCTCACCATTATATATATATATTTTAACTTGTCAGCTCATC
 TATGGAAACTACTCAGGTGGTATGCTGTTTGAAGCCTCATCTTCTACATGAAAATTATGGGCATTTGTCCCAATGAT
 TTTGTTTCAGCTGTTCTGTAGGCTGCATAACCACTCTGATATTTAGGTATCTGCTATTTTATTATCTTAAAGACAAAT
 TAATTTAATTGCATGTGCTAGGGAAAAGCTACCATGTACATTCACCCCAAGTAAATAGAATCCTAGATGAATCCTAGAA
 AAATAATCCCTAAGCAGATAGGTAGACAGAGGTAAACATTCACATGATTTAGCTCTCTAGCTCTTGCACTCTGAACATT

FIGURE 3 (cont'd)

CTTGCTTTGGTTCTGACTTCTGGGA GCTTTGCATTTCTCCTATAGATCTG TTAAGGGAACCAAGGGGTCATTG
GGGCAAAGCATTTGTTTCTCAAAGCTCCTTGATTAAGAGAAAGAACAGAAATTTGCACAGAAGATAGTGTCAAGGAGTG
AGAAAGTTTGTTTGAGGGCAGTAGCTCAGTGTGGAAGAAAATCCTGAAGTTTCTGTTGAAGCCATACAATGTTCTATGG
GGTACTCTCTAAGACATTCTCTGAGGTGTGTGAGGAAGTCACTACTCCTAGCCTTTGTTAAGATGTAATTTTAAATAT
TCAGTTATGGTACTATGTTTGCAACTCTCGTCTTATCACAATGCCTCAGTAGTTTGTTCCCTTAGAAACATTTAGATGT
GCACAAATTAATCTTTTATATATCTAAAGGTTTTTCTATCATGCATTGGATTGCTCAGAATAAAGTGTCTGTTAGACTT
CGTTTTGGTAAATAAATTCTCCATAATGTAGATTAATAATATAAAAGTCTTTAATGACACAATATATCTATATAGCCTC
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GCCGC

FIGURE 3 (cont'd)

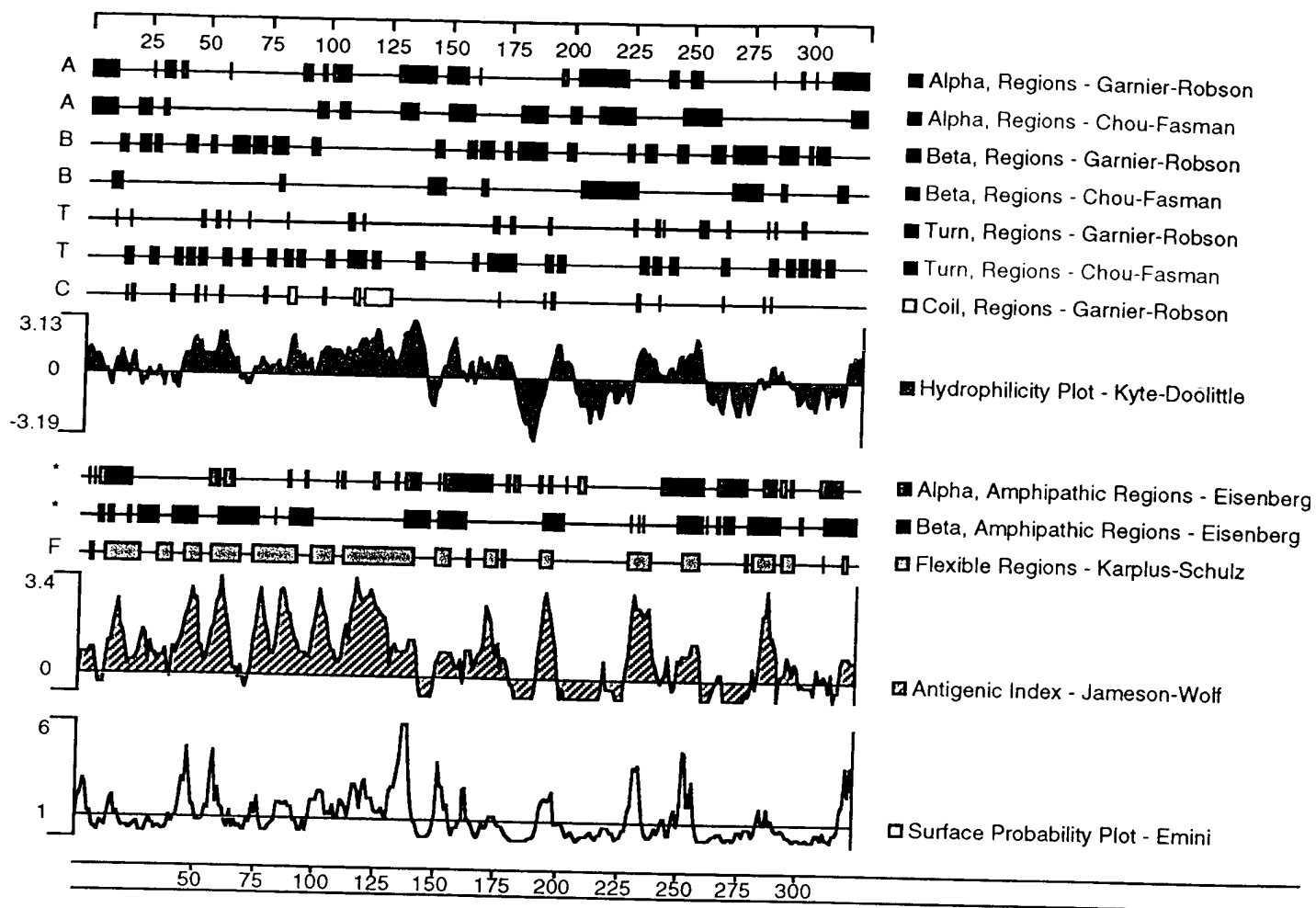


FIGURE 4

														M	L	K	S	C	S
GTCGACCCACGCGTCCGGGCGAATCTGTATTTCCAGTTAACTGCTCAGAAGAGAG														ATG	CTG	AAG	AGC	TGT	AGT
R	A	S	F	S	P	S	V	R	K	P	P	L	I	L	R	R	L	L	S
CGT	GCA	TCC	TTC	TCA	CCC	TCC	GTT	AGA	AAG	CCT	CCT	CTC	ATC	CTC	AGA	AGA	CTA	CTG	TCA
E	D	V	G	M	D	I	P	F	E	E	G	V	L	S	P	S	A	A	D
GAG	GAT	GTA	GGA	ATG	GAC	ATC	CCC	TTT	GAA	GAG	GGC	GTG	CTG	AGT	CCC	AGT	GCT	GCA	GAC
M	R	P	E	P	P	N	S	L	D	L	N	D	T	H	P	R	R	I	K
ATG	AGG	CCT	GAA	CCT	CCT	AAT	TCT	CTG	GAT	CTT	AAT	GAC	ACT	CAT	CCT	CGG	AGA	ATC	AAG
L	T	A	P	N	I	N	L	S	L	D	Q	S	E	G	S	I	L	S	D
CTC	ACA	GCC	CCA	AAT	ATC	AAT	CTT	TCT	CTG	GAC	CAA	AGT	GAA	GGA	TCT	ATT	CTC	TCT	GAT
D	N	L	D	S	P	D	E	I	D	I	N	V	D	E	L	D	T	P	D
GAT	AAC	TTG	GAC	AGT	CCA	GAT	GAA	ATT	GAC	ATC	AAT	GTG	GAT	GAA	CTT	GAT	ACC	CCC	GAT
E	A	D	S	F	E	Y	T	G	H	G	K	S	L	S	W	Q	G	Q	S
GAA	GCA	GAT	TCT	TTT	GAG	TAC	ACT	GGC	CAT	GGT	AAG	TCA	CTA	AGT	TGG	CAA	GGC	CAA	AGT

*
TAA

ATGCTAAATAAGTAAAAGATTTTCTAACAGACCTCTCATTTTTTGTGCCAGTGGATCCTTTTTTGTGATTTCTAGAAGCTT
CTGTTTTTATTTTACAGGTATAGGTGGCCATGATTGACAGTTTGGAGCCTGACAGAGAAAGTATGGGTCACAGAGGCCAT
ACATAACCATTGCTCTTTATTAACCCCCACTCTGTGCTAGCATTTATGCTAGGCACTGGGGCTGAGGGAAGACTGTTAC
ATGCTGTGTTACAAGAAACCTGGGGCTGGGTTTGCAGGGGAAGAGAATTTAATCAGGATGATAAAATTTGAAGAAGAGA
AATCAGAGCTTGCCAATTTCTTGTATAAGTTCCCACTATCTGCAATGTTCTTTTCCCCAGATCCTTACGTGACTGACTC
CTTCTCTTTATTTACAGATGTTAATCAGATGTCACCTCCTCAGAGAAGTCTTCCTTGACCTCTGTAATCAAAGATGCTTCC
CACTTCCCGACTCCCACCACCTAGTCACTCTCTGTCCCAGTGTTTATTTTATTTTCCACGTATCACTAATTCAAATTGT
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AGATAATTAAAAGTTTTTACAGATCATCCAAGACTGACACTCCTGATATGAACTTCAGTCTTTCTTTAGTTCTTTCTCTTA
CTCTATGAAATCTGGTTTAAGAAATATGTACAAATACAATCATTTTTTTTTTAAATGGCATTATGTAGTTTCTGTTTCAG
TTCTAGCCAGGGTGGAAATTTCTCTGAAGTTATAATATTTGAAAGTGAAAGCGAGAGAGTCTGGGACACAGCTATTGCTTT
TATTCATTTTTTAAATTCACGCAATCTTAAAAGCAATACAGTGCCACAATTAAGTGGTGGCCTGACTTTTAGAGACATG
CTAATTCTAGCAGTTCCACTCCTAGAAGAGCATAATTAGAAAATTCACCAAATTAGCTAATTATTTCAACCAATGGTCA
TTGAGCCGACATGAGCAGTGCAGTTCAGACTCTACCTTGACAGAGCTTAAGGCTTTATTTTCTCAAAAAGGAAATGGCT
AAACGACTTGTTTTATAGTCTATTATGCTTAAGTAGAGTTTTTTTTTTTTTCCATAAGTTATTGGGGTACAGGTGGTATT
TGGTTACATGAGTAAGTTCTTTAGTGTAAGTAGAGATTTTATATTGCATTTTTTATCATGTGTGAATTTCTGTAGTTATC

FIGURE 5

TGGGTAGTTGATTCTGTAGGTTGAAATACACAAATAGGAGGTGAAAGAAGGTCTGGAATTTGTACTATTTCTGTGTCATC
CCAGAGAGTCTTCAGCAGCTCCTCTATCCATCCCAGTTGCCCCCTACCAGCTCCTGCTCCTTTCCCTGCTAATATATTG
ACCAAATCCCACAGAAGACTGTGGCATGACCCAACTGGCCCCCTCTCTTGCCCTCCGGTATTTGCTTCCTTTTTGTTCAGGA
GAGCTTTGTACACCACATCTGAACCTTTTATTTTTTAAACATAGTAAACTGTGAGCAAAGCAGTGGTGGCTGGGCAA
GCTGGTAATTAACACTGCCACTTGCTGACATGGCTCTTTTAATGTAGTTAACATAGCTGTGTTGAAAGAACCAGTTTAA
TGGCCACAACCCTGTTTTAGGTCTTAAATGCAAAGGACAGAATTGTAAACTAAGTTGAATTTTTTAAATCTACCTTAATT
TTCAAATGAAAGATATATAGTCAGAGGTTGAAACTTTGAAAACACAAAGTGCCTCTGAATAGCTATATTTTGTAACAT
GAGGACATGGATAAGTGACTGTATAAGAGGGTTGGATTATAAATATGTTTGAGTTCTGAAGTATGAAATAAATGCTTGA
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GTATATTATATACCTCATTATATTATATAATTCATTATATAGTTTTTCATTTAATTTATTTTCATTTTATAACTAGAACAA
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CCAGTGAATATGCTAACAAATGAATGGGAAAGGGTCTGTTACCAGATTGGACTTACATACTTGAAGCCAAACATGATAGC
TCTTGCTCACATTTAGGCCTCTTTTTATCCAGTTTTCTGACTTGCGGGAGACTCTAAAAAAAAAAAAAAAAAGGGCGGCC
GC

FIGURE 5 (cont'd)

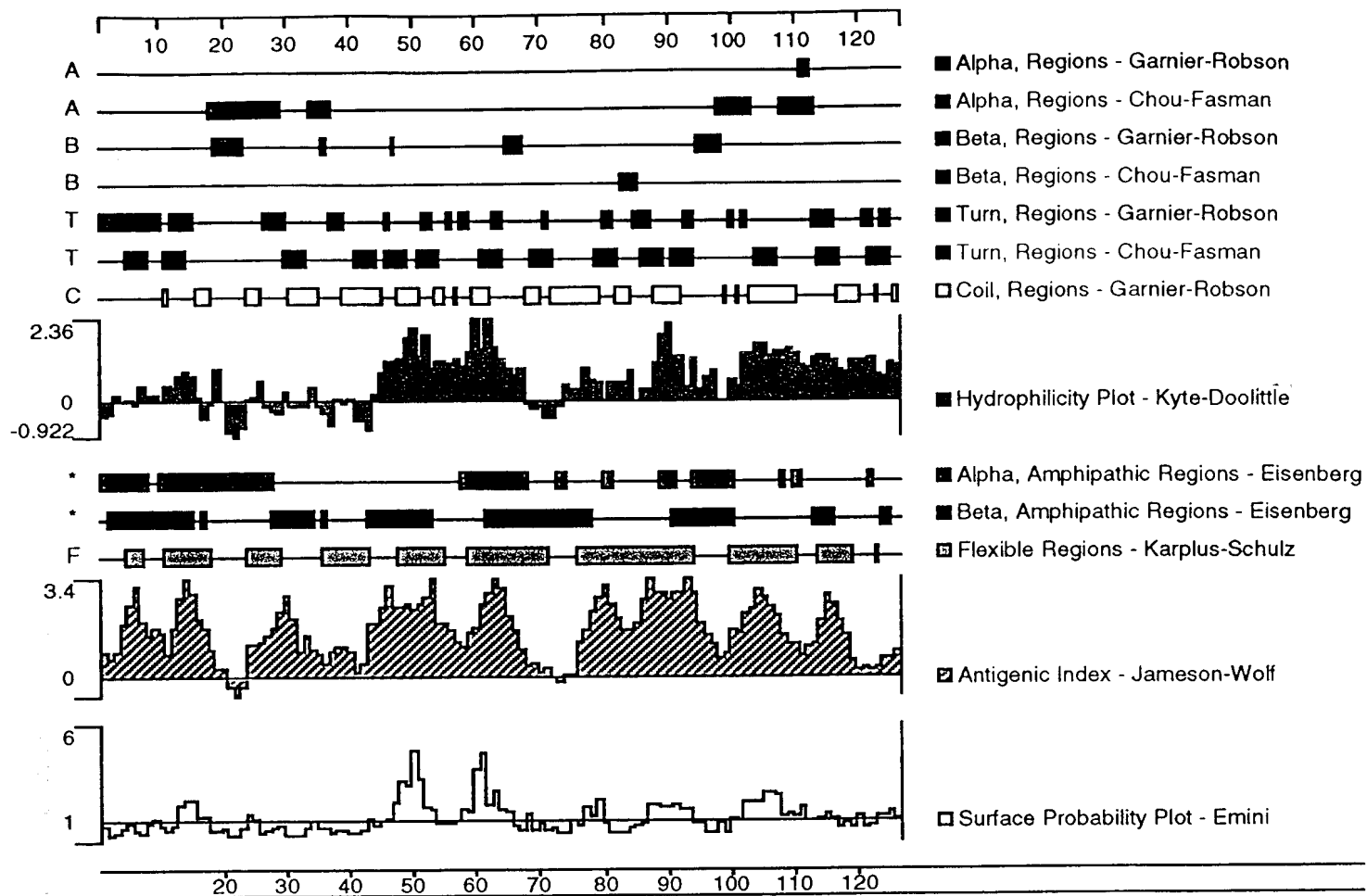


FIGURE 6

>PF00335|transmembrane4 4 transmembrane segments integral membrane proteins

Score: 1.28 Seq: 253 293 Model: 192 232
CMekIqdWlhnnNfIIIagIciGIafIEilgMvFSMCLCRqI
C++ I+ L++N+ + +++ + +L ++ + +++I
human 253 CYQMIDRRRLRKNLKSIIIVHPSWFIRTVLAI SRPFISVKFI 293

FIGURE 7

FIGURE 9

GAP of: nip2b.pep check: 7307 from: 1 to: 371

NIP2B

to: nip2c.pep check: 3344 from: 1 to: 322

NIP2C Athda22f7

Symbol comparison table: /usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.comp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 871 Length: 375
Ratio: 2.705 Gaps: 4
Percent Similarity: 69.182 Percent Identity: 58.805

Match display thresholds for the alignment(s):
= IDENTITY
: = 2
- = 1

nip2b.pep x nip2c.pep

```
1 .MGTTEATLRMENVDVKEEWQDEDI.PRPLPEETGVELLGSPVEDTSSPPN 49
  || : ||| | : |||
1 MEEETEFLLELGTRISRPNGLLSEDVGMDFEEGV.LSPSAADMRPEPPN 49
50 TLNFNGAHRKRKTI.VAPEINISLDQSEGSLLSDDFLDTPDDLDINVDDIE 99
  .| | : | | | | : | | | | : | | | | : | | | | : | |
50 SLDLNDTHPRRIKLTAPNINLSLDQSEGSILSDDNLDSPDEIDINVDELD 99
100 TPDETDLSLEFLGNGNELEWEDDTPVATAKNMPGDSADLFGDGTTEGSA 149
  ||| | | : | | ||| | : | | : | | :
100 TPDEADSFYEYTGHD.....PTANKDSGQESISIPEYTAEEERED 138
150 NGRLWRTVIIGEQEHRIDLHMIRPYMKVVTHG...GYGEGLNAIIVFAA 196
  | | | | : | | | | | : | | : | | : | | | | | | | |
139 N.RLWMTVVIGEQEQRIDMKVIEPYRRVISHGGDSGYGDGLNAIIVFAA 187
197 CFLPDSSLPDYHYIMENLFLYVISSLELLVAEDYMIVYLNATPRRRMPG 246
  ||| | | | | | | | | | | | | | | | | | | | | | | |
188 CFLPDSSRADYHYVMENLFLYVISTLELMVAEDYMIVYLNATPRRRMPG 237
247 IGWLKKCYQMIDRRRLRKNLKSIIIVHPSWFIRTVLAI SRPFISVKFINKI 296
  : | | : | | | | | | | | | | | | | | | | | | | | |
238 LGWMKKCYQMIDRRRLRKNLKSFIIVHPSWFIRTILAVTRPFISSKFSSKI 287
297 QYVHSLEDLEQLIPMEHVQIPDCVLOYEEERLKRRESARPOPEFVI.PRS 346
  .| | .| | : | | | | : | | : | | : | | : | |
288 KYVNSLSLSGLIPMDCIHIPESIINIDLKLEKP..... 322
```

FIGURE 11

NIP2C Athda22f7

NIP2A | U15173 Homo sapiens BCL2/adenovirus E1B 19kD-interacting protein 2 (BNIP2)

Symbol comparison table: /usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003

Quality:	806	Length:	331
Ratio:	2.567	Gaps:	6
Percent Similarity:	<u>67.541</u>	Percent Identity:	<u>57.705</u>

```

Match display thresholds for the alignment(s):
      | = IDENTITY
      : = 2
      : = 1

```

nip2c.pcp x nip2a.pcp

1 MEEETEFLEIGTRISRPNGLLSEVDGMDIPFEEGVLSPSAADMPE.PPN 49
1MEGVELKEEWQDEDFPIPLPEDDSTEADILAITGPEDQPG 40
50 SLDLNDTHPRRIKLTAPNTNLSLDQSECSILSDDNLDSPDEIDINVDELD 99
41 SLEVNGNKVRK.KLMAPDISLTHDPSDGSVLSDD.LDESCEIDL..DGLD 86
100 TPDE.ADSFEYTGHDPTANKDSCQSESIPEYTAEEEREDNRLWMTVVIG 148
87 TPSENSNEFEWEDDLPKPKTTEVIRKGSITEYTAEEKEDGRRWRMFRIG 136
149 EQEQRIDMKVIEPYRRVLSHGGSGLNGLNAILVFAACFLPDSSRADY 198
137 EQDHRVDMKAIEPYKKVISHG...GYGDLNAILVFAVCFMPESSQPNY 183
199 HYVMENLFLYVISTLELMVAEDYMIIVYLNGATPRRRMPGLGWMKKCYQMI 248
184 RYLMNDNLFKYVIGTLELLVAENYMIIVYLNGATTTRRKMPSLGWLKCYQOI 233
249 DRRLRKNLKSFIIVHPSWFIRTILAVTRPFISSKFSSKIYVNSLSELSG 298
234 DRRLRKNLKSILTIVHPSWFIRTILAVTRPFISSKFSQKIRYVFNLAELAE 283
299 LIPMDCIHIPESIINIDLKLEKP..... 322
284 LVPMEYVGIPCEIKQVDQELNGKQDEPKNEQ 314

FIGURE 12